

# Report

	assembly
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	1995454
Total length (>= 5000 bp)	1990481
Total length (>= 10000 bp)	1982468
Total length (>= 25000 bp)	1968224
Total length (>= 50000 bp)	1968224
# contigs	6
Largest contig	1890766
Total length	1995454
Reference length	1905333
GC (%)	52.11
Reference GC (%)	52.30
N50	1890766
NG50	1890766
N75	1890766
NG75	1890766
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1905010
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	85879
Genome fraction (%)	100.000
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	18.11
# indels per 100 kbp	76.99
Largest alignment	1244267
Total aligned length	1909546
NA50	1244267
NGA50	1244267
NA75	646498
NGA75	646498
LA50	1
LGA50	1
LA75	2
LGA75	2

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

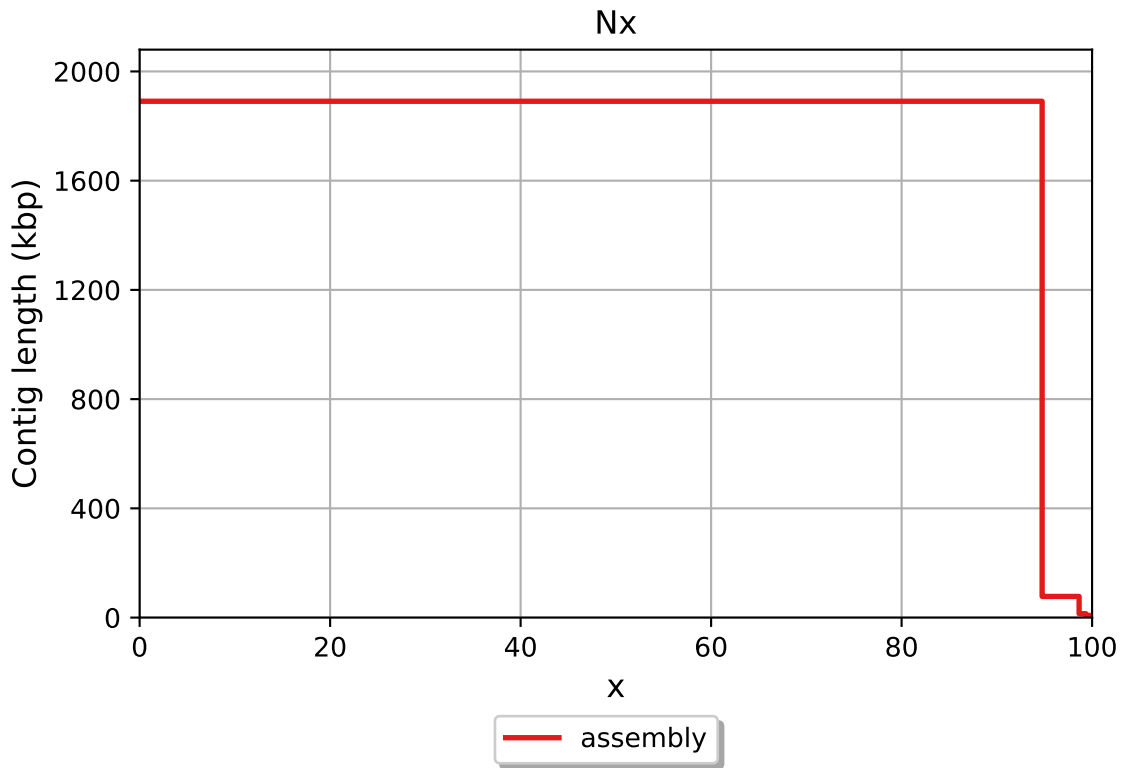
	assembly
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	1905010
# possibly misassembled contigs	3
# possible misassemblies	3
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	345
# indels	1467
# indels (<= 5 bp)	1463
# indels (> 5 bp)	4
Indels length	1580

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

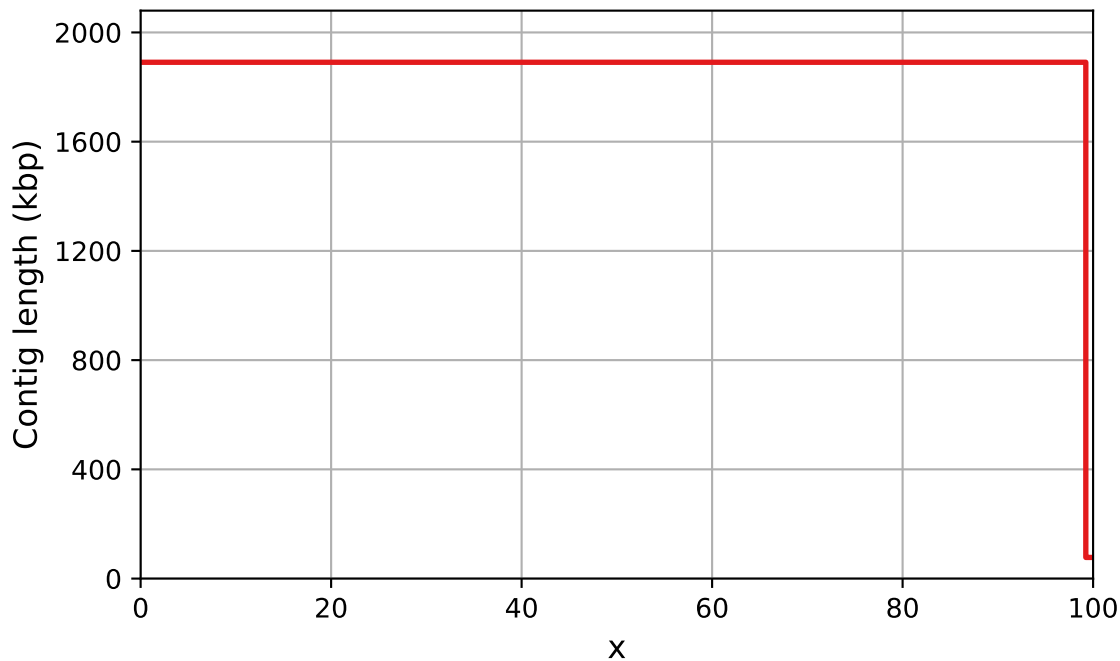
## Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	85879
# N's	0

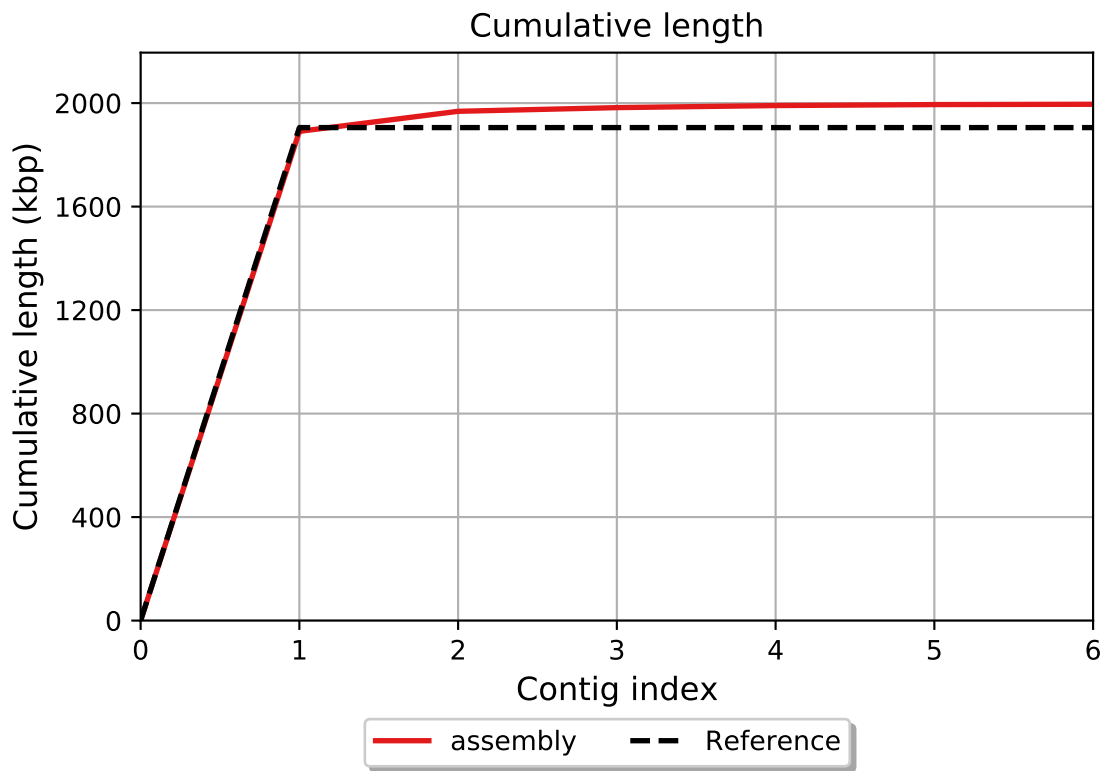
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



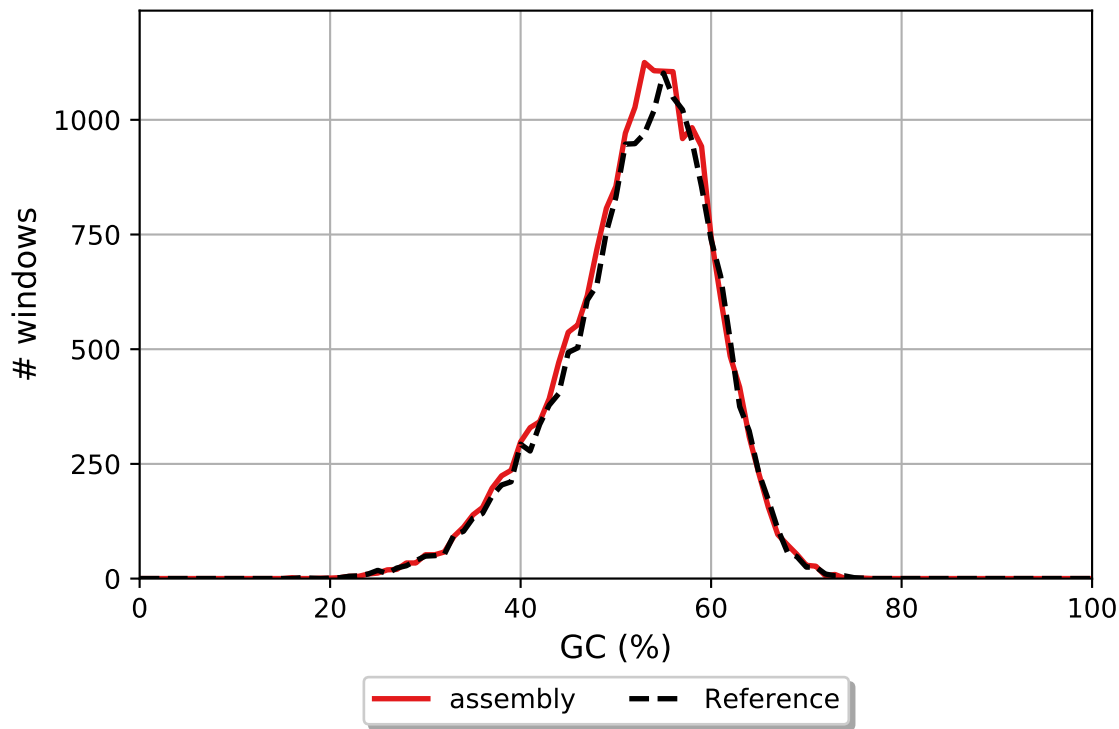
NGx



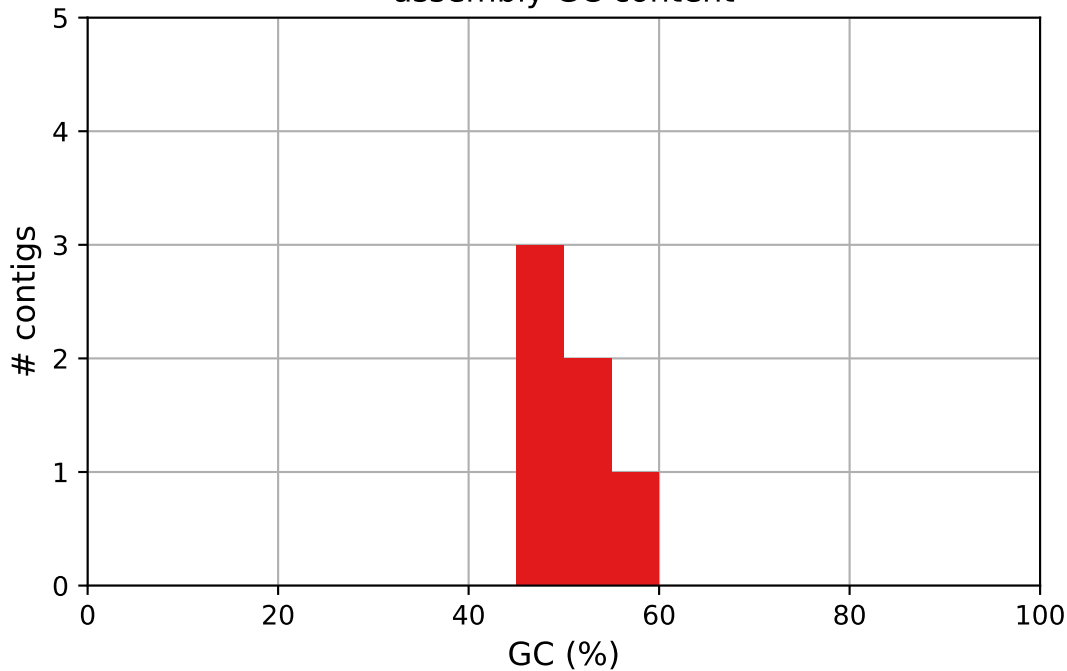
— assembly



## GC content



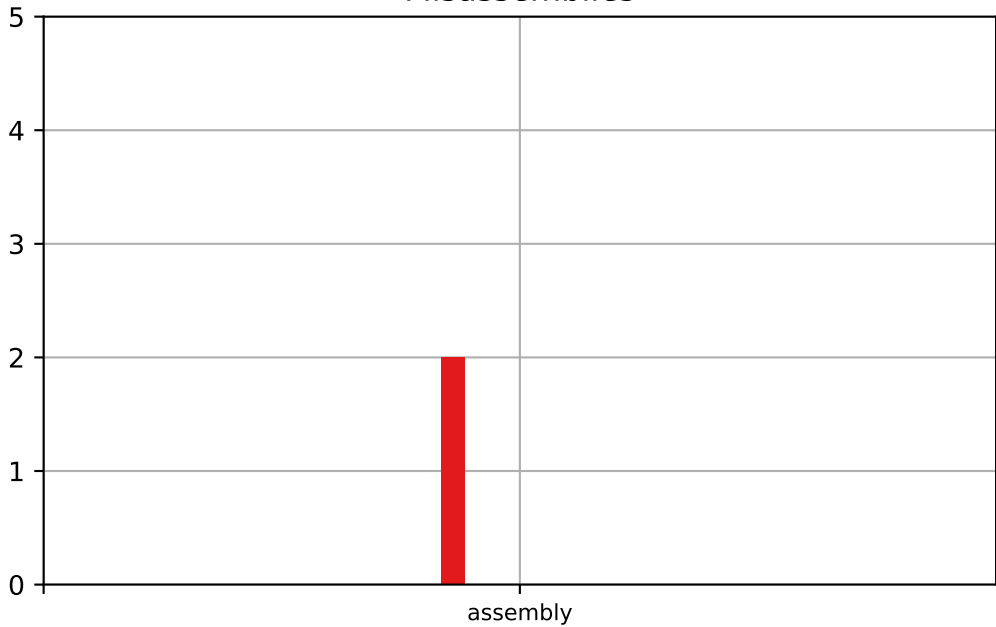
assembly GC content



assembly

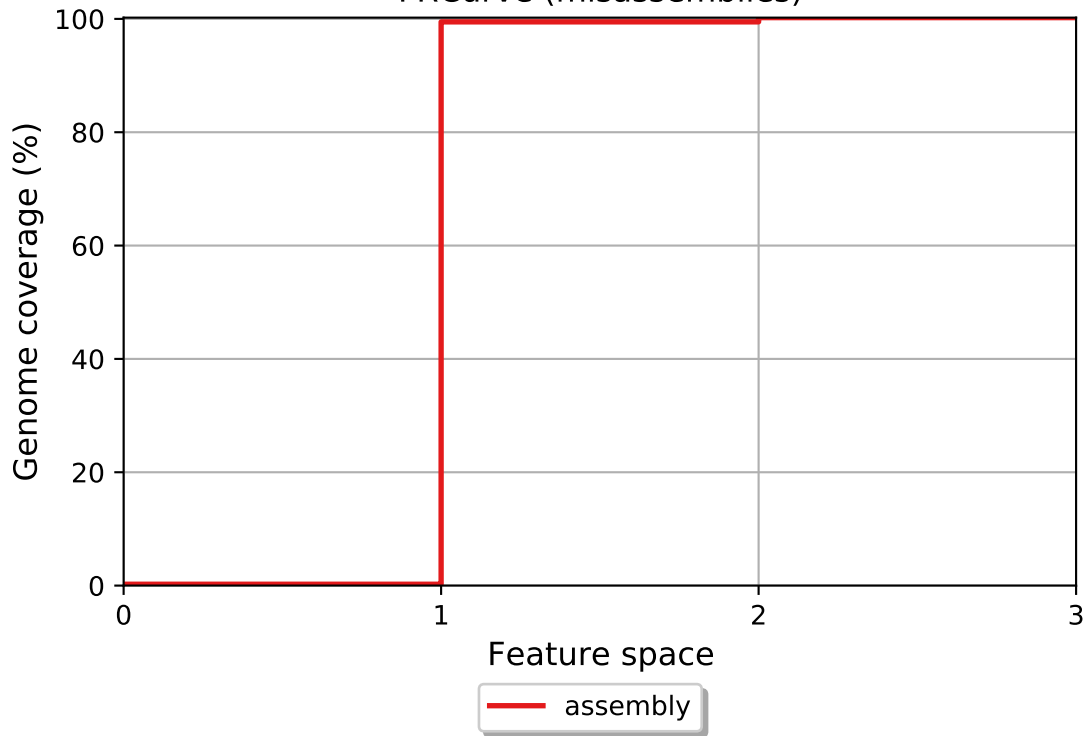


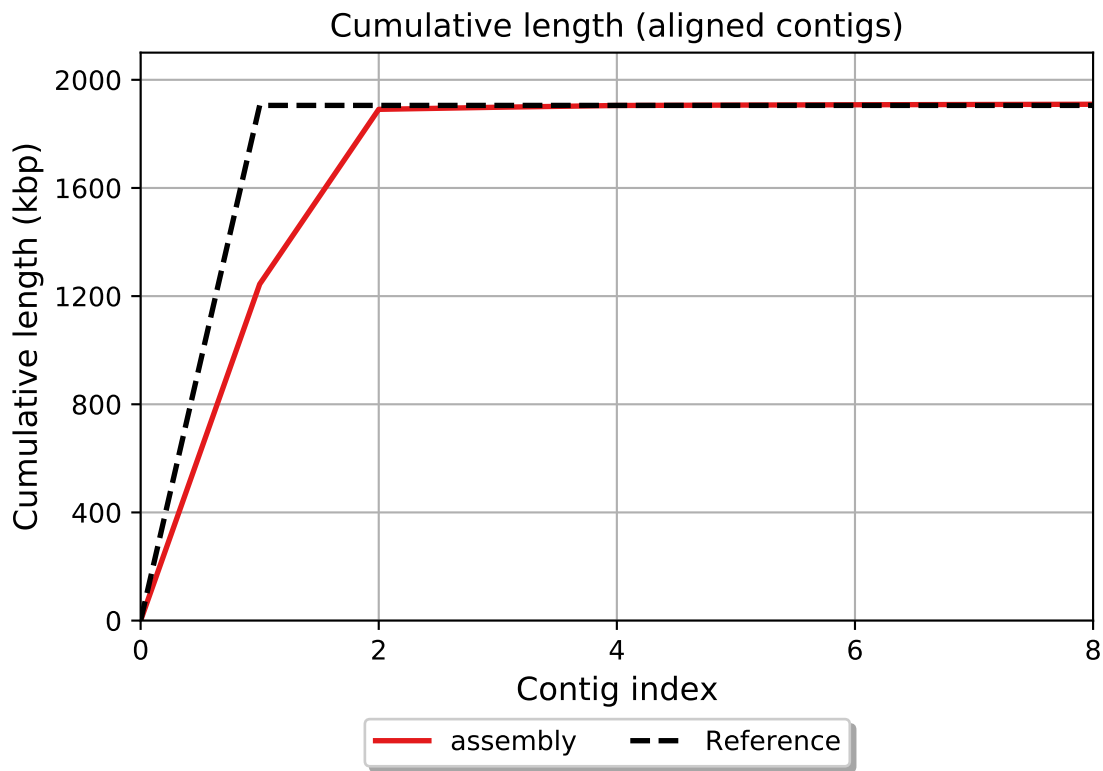
## Misassemblies



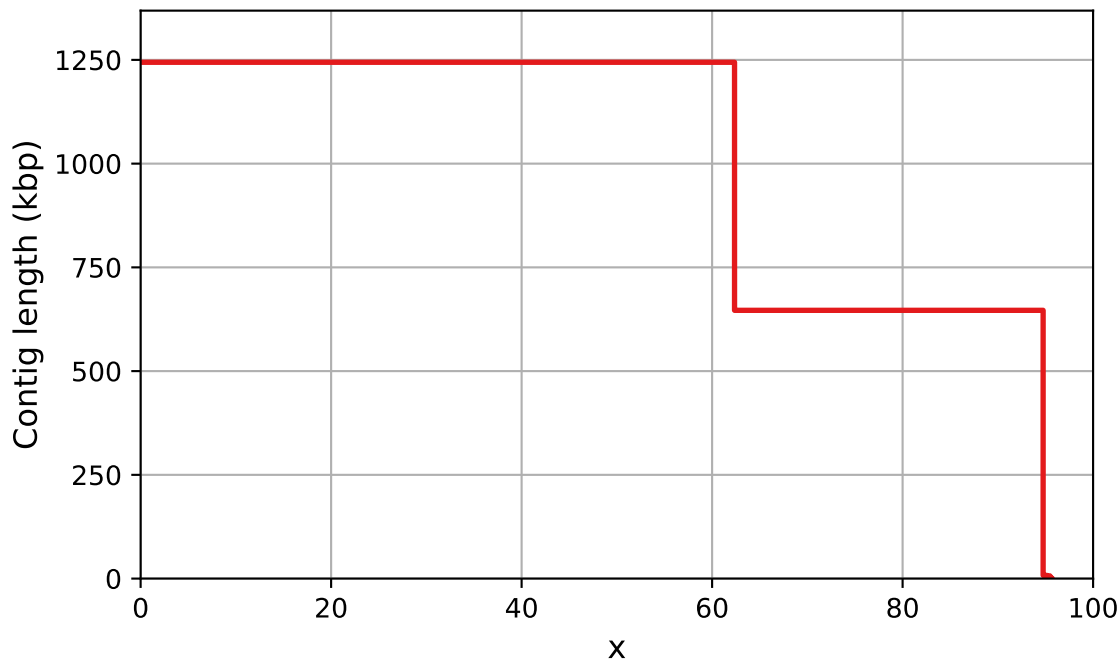
 # relocations

FRCurve (misassemblies)



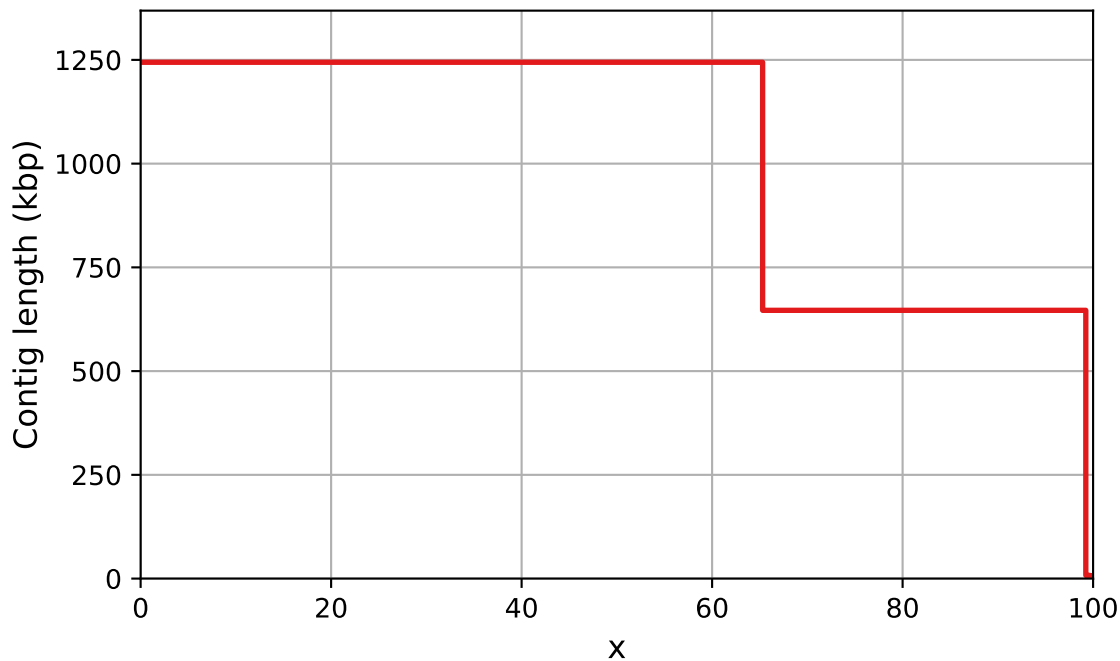


NAx



— assembly

# NGAx



— assembly